

Abstract

Methods and compositions are provided for the identification of expression signatures in ER+ breast cancer cases, where the signatures correlate with responsiveness, or lack thereof, to tamoxifen treatment. The signature profiles are identified based upon sampling of reference breast tissue samples from independent cases of breast cancer and provide a reliable set of molecular criteria for predicting the efficacy of treating a subject with ER+ breast cancer with tamoxifen. Additional methods and compositions are provided for predicting tamoxifen responsiveness in cases of ER+ breast cancer by use of three biomarkers. Two biomarkers display increased expression correlated with tamoxifen response while the third biomarker displays decreased expression correlated with tamoxifen response.